



SEQUENCE LISTING

<110> GALZI, JEAN-LUC
ALIX, PHILIPPE

<120> USE OF A FLUORESCENT PROTEIN FOR DETECTING INTERACTION
BETWEEN A TARGET PROTEIN AND ITS LIGAND

<130> 0508-1053-1

<140> 10/776,330
<141> 2004-02-12

<150> 09/445,205
<151> 2000-01-07

<150> PCT/FR98/01136
<151> 1998-06-04

<150> FR 97/06977
<151> 1997-06-05

<160> 25

<170> PatentIn Ver. 3.2

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<210> 1
<211> 798
<212> DNA
<213> Aequorea victoria
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<220>
<221> CDS
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<400> 1
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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc aac cac atg aag 240
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160	480
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175	528
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 180 185 190	576
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205	624
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 215 220	672
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tac Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Tyr 225 230 235 240	720
tca gat ctc gag ctc aag ctt cga att ctg cag tcg acg gta ccg cgg Ser Asp Leu Glu Leu Lys Leu Arg Ile Leu Gln Ser Thr Val Pro Arg 245 250 255	768
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<210> 2	
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<212> PRT	
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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Tyr
 225 230 235 240

Ser Asp Leu Glu Leu Lys Leu Arg Ile Leu Gln Ser Thr Val Pro Arg
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Ala Arg Asp Pro Pro Asp Leu Asp Asn
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<210> 3

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic spacer sequence

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 1 5

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<210> 4
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic cyclopeptide

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1 5

<210> 5
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
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<400> 5
ggtcgccacc ctgtacaaga agggcgagg

29

<210> 6
<211> 36
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 6
cacgagagga tgtacaacct cgagcgcaca gtcacc

36

<210> 7
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 7
gtacccagac accagctagc agatctgaag cttcgccatc aggc

44

<210> 8
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<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

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<210> 9
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
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<210> 10
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<400> 10
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<210> 11
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<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

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<210> 12
<211> 28
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

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<400> 12
cctgctgtct cagatctcat caccgtcc                                28

<210> 13
<211> 47
<212> DNA
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<400> 13
cagatcatta gttgtacagg aaagatcttg aggatcctgg agtgaag          47

<210> 14
<211> 29
<212> DNA
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<220>
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<400> 14
ggcccaagct tatgtcagga tccggggat                                29

<210> 15
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<212> DNA
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<400> 15
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<210> 16
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<400> 16
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<210> 17
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<213> Artificial Sequence

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<220>
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<400> 17
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<210> 18
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<212> DNA
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<400> 18
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tgctgcttcg cctacatt 78

<210> 19
<211> 78
<212> DNA
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<210> 20
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<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

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<210> 21
<211> 69
<212> DNA
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<220>
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<210> 22
<211> 50
<212> DNA
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<220>
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<210> 23
<211> 21
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 23
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<210> 24
<211> 41
<212> DNA
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<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 24
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<210> 25
<211> 43
<212> DNA
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<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 25
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